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A/ Figure 1 provides a sequence alignment of ER- α (SEQ ID NO:1) with ER- β (SEQ ID NO:2) covering the ordered extent of ER- β . The numbering scheme used was chosen to be consistent with ER- α , such that the first ordered ER- β residue, 311 is residue 263 in the full length protein. Residues in helix 12 are underlined. The (*) symbols indicate the altered binding site residues.

Please attach at the end of the application pages 1-3 of the Sequence Listing (attached hereto as Exhibit E).

REMARKS

By this Amendment, applicants have amended the specification to refer to sequence identifiers, as required by the Sequence Rules, and to add the Sequence Listing. The amendments to the specification are supported by the application as originally filed. Accordingly, entry of the amendments to the specification is respectfully requested.

Compliance with Sequence Rules

The August 31, 2001 Notice to File Missing Parts of Nonprovisional Application (Exhibit A) indicated that the application did not comply with the Sequence Rules. In response thereto, applicants attach herewith Exhibit E, consisting of pages 1-3 of the Sequence Listing. Also enclosed is a computer-readable form containing the Sequence Listing (Exhibit F). Additionally, the specification has been amended to refer to the sequence identifiers, as required by the Sequence Rules.

The undersigned attorney hereby certifies that the information recorded in computer-readable form is identical to the written Sequence Listing, is supported by the application as filed, and does not introduce new matter into the application as filed. In